



#4

## SEQUENCE LISTING

<110> Mack, David  
Gish, Kurt  
Wilson, Keith

<120> NOVEL METHODS OF DIAGNOSING COLORECTAL CANCER, COMPOSITIONS AND METHODS  
OF SCREENING FOR COLORECTAL CANCER MODULATORS

<130> A-69796/DJB/JJD

<140> US 09/733,757

<141> 2000-12-08

<160> 3

<170> PatentIn version 3.0

<210> 1

<211> 2103

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)..(2103)

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Met Leu Ser Ser Thr Asp Phe Thr Phe Ala Ser Trp Glu Leu  
1 5 10  
gtg gtc cgc gtt gac cat ccc aat gaa gag cag cag aaa gac gtc aca 159  
Val Val Arg Val Asp His Pro Asn Glu Glu Gln Gln Lys Asp Val Thr  
15 20 25 30  
ctg aga gta tct gga gac ctt cac gtt gga gga gtg atg ctc aag tta 207  
Leu Arg Val Ser Gly Asp Leu His Val Gly Gly Val Met Leu Lys Leu  
35 40 45  
gta gaa cag atc aat ata tcc caa gac tgg tca gac ttt gct ctt tgg 255  
Val Glu Gln Ile Asn Ile Ser Gln Asp Trp Ser Asp Phe Ala Leu Trp  
50 55 60  
tgg gaa cag aag cat tgc tgg ctt ctg aaa acc cac tgg acc ctg gac 303  
Trp Glu Gln Lys His Cys Trp Leu Leu Lys Thr His Trp Thr Leu Asp  
65 70 75  
aaa tat ggg gtc cag gca gat gca aag ctt ctc ttc acc cct cag cat 351  
Lys Tyr Gly Val Gln Ala Asp Ala Lys Leu Leu Phe Thr Pro Gln His  
80 85 90  
aaa atg ctg cgc ctt cgt ctg ccg aat ttg aag atg gtg agg ttg cga 399  
Lys Met Leu Arg Leu Arg Leu Pro Asn Leu Lys Met Val Arg Leu Arg  
95 100 105 110

gtc agc ttc tca gct gtg gtt ttt aaa gct gtc agt gat atc tgc aaa Val Ser Phe Ser Ala Val Val Phe Lys Ala Val Ser Asp Ile Cys Lys 115 120 125	447
atc ctg aat att aga aga tca gaa gag ctt tcc ttg tta aag ccg tct Ile Leu Asn Ile Arg Arg Ser Glu Glu Leu Ser Leu Leu Lys Pro Ser 130 135 140	495
ggt gac tat ttt aag aag aag aag aaa aaa gac aaa aat aat aag gaa Gly Asp Tyr Phe Lys Lys Lys Lys Lys Lys Lys Asp Lys Asn Asn Lys Glu 145 150 155	543
ccc ata att gaa gat att cta aac ctg gag agt tct cca aca gct tca Pro Ile Ile Glu Asp Ile Leu Asn Leu Glu Ser Ser Pro Thr Ala Ser 160 165 170	591
ggt tca tca gta agt cct ggt tta tac agt aaa acc atg acc cct ata Gly Ser Ser Val Ser Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Ile 175 180 185 190	639
tat gac ccc atc aat gga aca cca gca tca tcc acc atg act tgg ttc Tyr Asp Pro Ile Asn Gly Thr Pro Ala Ser Ser Thr Met Thr Trp Phe 195 200 205	687
agt gac agc cct ttg acg gaa caa aac tgc agc atc ctc gca ttc agc Ser Asp Ser Pro Leu Thr Glu Gln Asn Cys Ser Ile Leu Ala Phe Ser 210 215 220	735
caa ccc ccc cag tcc cca gaa gca ctt gcg gat atg tac cag cct cgg Gln Pro Pro Gln Ser Pro Glu Ala Leu Ala Asp Met Tyr Gln Pro Arg 225 230 235	783
tct ctg gtt gat aaa gcc aag ctc aat gca ggt tgg cta gac tcc tca Ser Leu Val Asp Lys Ala Lys Leu Asn Ala Gly Trp Leu Asp Ser Ser 240 245 250	831
cgc tcc ctt atg gaa caa gcc atc caa gag gat gag cag ctg ctc tta Arg Ser Leu Met Glu Gln Gly Ile Gln Glu Asp Glu Gln Leu Leu Leu 255 260 265 270	879
cga ttt aaa tat tat tct ttc ttc gac ttg aat cct aaa tat gat gct Arg Phe Lys Tyr Tyr Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala 275 280 285	927
gtc cga ata aac caa ctc tat gag caa gcc agg tgg gcc att ctc tta Val Arg Ile Asn Gln Leu Tyr Glu Gln Ala Arg Trp Ala Ile Leu Leu 290 295 300	975
gaa gaa att gat tgc aca gag gaa gaa atg ttg atc ttt gca gct cta Glu Glu Ile Asp Cys Thr Glu Glu Glu Met Leu Ile Phe Ala Ala Leu 305 310 315	1023
cag tac cac att agc aaa ctg tcg ttg tct gct gaa aca cag gat ttt Gln Tyr His Ile Ser Lys Leu Ser Leu Ser Ala Glu Thr Gln Asp Phe 320 325 330	1071
gca gcc gag tcc gag gtt gat gaa ata gaa gcg gcg ctt tct aat ttg Ala Gly Glu Ser Glu Val Asp Glu Ile Glu Ala Ala Leu Ser Asn Leu 1119	1119



aaa gga agc aaa aaa gat gac att ctg gga gtt tca tat aac agg ttg 1839  
 Lys Gly Ser Lys Lys Asp Asp Ile Leu Gly Val Ser Tyr Asn Arg Leu  
 575 580 585 590

att aaa att gat gca gcc acc ggg att cca gtg aca aca tgg aga ttc 1887  
 Ile Lys Ile Asp Ala Ala Thr Gly Ile Pro Val Thr Thr Trp Arg Phe  
 595 600 605

aca aat atc aaa cag tgg aat gta aac tgg gaa acc cgg cag gtg gtc 1935  
 Thr Asn Ile Lys Gln Trp Asn Val Asn Trp Glu Thr Arg Gln Val Val  
 610 615 620

atc gag ttt gac caa aac gtc ttt act gct ttc acc tgc ctg agt gca 1983  
 Ile Glu Phe Asp Gln Asn Val Phe Thr Ala Phe Thr Cys Leu Ser Ala  
 625 630 635

gat tgc aag att gtg cac gag tac att ggc ggc tac att ttc ttg tcc 2031  
 Asp Cys Lys Ile Val His Glu Tyr Ile Gly Gly Tyr Ile Phe Leu Ser  
 640 645 650

acc cgc tcc aag gac cag aat gaa aca ctc gat gag gac ttg ttc cac 2079  
 Thr Arg Ser Lys Asp Gln Asn Glu Thr Leu Asp Glu Asp Leu Phe His  
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Val Ser Gly Asp Leu His Val Gly Gly Val Met Leu Lys Leu Val Glu  
 35 40 45

Gln Ile Asn Ile Ser Gln Asp Trp Ser Asp Phe Ala Leu Trp Trp Glu  
 50 55 60

Gln Lys His Cys Trp Leu Leu Lys Thr His Trp Thr Leu Asp Lys Tyr  
 65 70 75 80

Gly Val Gln Ala Asp Ala Lys Leu Leu Phe Thr Pro Gln His Lys Met  
 85 90 95

Leu Arg Leu Arg Leu Pro Asn Leu Lys Met Val Arg Leu Arg Val Ser  
 100 105 110

Phe Ser Ala Val Val Phe Lys Ala Val Ser Asp Ile Cys Lys Ile Leu  
 115 120 125

Asn Ile Arg Arg Ser Glu Glu Leu Ser Leu Leu Lys Pro Ser Gly Asp  
 130 135 140

Tyr Phe Lys Lys Lys Lys Lys Lys Asp Lys Asn Asn Lys Glu Pro Ile  
 145 150 155 160

Ile Glu Asp Ile Leu Asn Leu Glu Ser Ser Pro Thr Ala Ser Gly Ser  
 165 170 175

Ser Val Ser Pro Gly Leu Tyr Ser Lys Thr Met Thr Pro Ile Tyr Asp  
 180 185 190

Pro Ile Asn Gly Thr Pro Ala Ser Ser Thr Met Thr Trp Phe Ser Asp  
 195 200 205

Ser Pro Leu Thr Glu Gln Asn Cys Ser Ile Leu Ala Phe Ser Gln Pro  
 210 215 220

Pro Gln Ser Pro Glu Ala Leu Ala Asp Met Tyr Gln Pro Arg Ser Leu  
 225 230 235 240

Val Asp Lys Ala Lys Leu Asn Ala Gly Trp Leu Asp Ser Ser Arg Ser  
 245 250 255

Leu Met Glu Gln Gly Ile Gln Glu Asp Glu Gln Leu Leu Leu Arg Phe  
 260 265 270

Lys Tyr Tyr Ser Phe Phe Asp Leu Asn Pro Lys Tyr Asp Ala Val Arg  
 275 280 285

Ile Asn Gln Leu Tyr Glu Gln Ala Arg Trp Ala Ile Leu Leu Glu Glu  
 290 295 300

Ile Asp Cys Thr Glu Glu Glu Met Leu Ile Phe Ala Ala Leu Gln Tyr  
 305 310 315 320

His Ile Ser Lys Leu Ser Leu Ser Ala Glu Thr Gln Asp Phe Ala Gly  
 325 330 335

Glu Ser Glu Val Asp Glu Ile Glu Ala Ala Leu Ser Asn Leu Glu Val  
 340 345 350

Thr Leu Glu Gly Gly Lys Ala Asp Ser Leu Leu Glu Asp Ile Thr Asp  
 355 360 365

Ile Pro Lys Leu Ala Asp Asn Leu Lys Leu Phe Arg Pro Lys Lys Leu  
 370 375 380

Leu Pro Lys Ala Phe Lys Gln Tyr Trp Phe Ile Phe Lys Asp Thr Ser  
 385 390 395 400

Ile Ala Tyr Phe Lys Asn Lys Glu Leu Glu Gln Gly Glu Pro Leu Glu  
 405 410 415

Lys Leu Asn Leu Arg Gly Cys Glu Val Val Pro Asp Val Asn Val Ala  
 420 425 430

Gly Arg Lys Phe Gly Ile Lys Leu Leu Ile Pro Val Ala Asp Gly Met  
 435 440 445

Asn Glu Met Tyr Leu Arg Cys Asp His Glu Asn Gln Tyr Ala Gln Trp  
 450 455 460

Met Ala Ala Cys Met Leu Ala Ser Lys Gly Lys Thr Met Ala Asp Ser  
 465 470 475 480

Ser Tyr Gln Pro Glu Val Leu Asn Ile Leu Ser Phe Leu Arg Met Lys  
 485 490 495

Asn Arg Asn Ser Ala Ser Gln Val Ala Ser Ser Leu Glu Asn Met Asp  
 500 505 510

Met Asn Pro Glu Cys Phe Val Ser Pro Arg Cys Ala Lys Lys His Lys  
 515 520 525

Ser Lys Gln Leu Ala Ala Arg Ile Leu Glu Ala His Gln Asn Val Ala  
 530 535 540

Gln Met Pro Leu Val Glu Ala Lys Leu Arg Phe Ile Gln Ala Trp Gln  
 545 550 555 560

Ser Leu Pro Glu Phe Gly Leu Thr Tyr Tyr Leu Val Arg Phe Lys Gly  
565 570 575

Ser Lys Lys Asp Asp Ile Leu Gly Val Ser Tyr Asn Arg Leu Ile Lys  
580 585 590

Ile Asp Ala Ala Thr Gly Ile Pro Val Thr Thr Trp Arg Phe Thr Asn  
595 600 605

Ile Lys Gln Trp Asn Val Asn Trp Glu Thr Arg Gln Val Val Ile Glu  
610 615 620

Phe Asp Gln Asn Val Phe Thr Ala Phe Thr Cys Leu Ser Ala Asp Cys  
625 630 635 640

Lys Ile Val His Glu Tyr Ile Gly Gly Tyr Ile Phe Leu Ser Thr Arg  
645 650 655

Ser Lys Asp Gln Asn Glu Thr Leu Asp Glu Asp Leu Phe His Lys Leu  
660 665 670

Thr Gly Gly Gln Asp  
675

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<220>  
<223> Cytokine receptor extracellular motif found in many species.

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<221> UNSURE  
<222> (3)..(3)  
<223> "Xaa" at position 3 can be any amino acid.

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Trp Ser Xaa Trp Ser  
1 5